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SEQUENCE LISTING

<110> SODE, Koji

<120> Glucose dehydrogenase beta-subunit and DNA encoding the same

<130> G780-0P1551

<141> 2003-04-25

<150> JP 2002-125353

<151> 2002-04-26

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 2467

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (258)..(761)

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<221> CDS

<222> (764)..(2380)

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<222> (2386)..(2466)

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tacgaatggc tgacacatgt aatggactat aaaaccatgt tccgttccgg aatgtgcgcg 180
tacatttcag gtccgcgccg atttttgaga aatatcaagc gtggtttcc cgaatccgg 240
gttcgagaga aggaaac atg cac aac gac aac act ccc cac tcg cgt cgc 290

Met His Asn Asp Asn Thr Pro His Ser Arg Arg

1

5

10

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cac	ggc	gac	gca	gcc	gca	tca	ggc	atc	acg	cg	cgt	caa	tgg	ttg	caa	338						
His	Gly	Asp	Ala	Ala	Ala	Ser	Gly	Ile	Thr	Arg	Arg	Gln	Trp	Leu	Gln							
15								20					25									
ggc	g	cg	ctg	g	cg	ctg	acc	g	ca	g	gc	ctc	acg	g	gt	tcg	ctg	aca	ttg	386		
Gly	Ala	Leu	Ala	Leu	Ala	Leu	Thr	Ala	Ala	Gly	Leu	Thr	Gly	Ser	Leu	Thr	Leu					
30								35					40									
cgg	g	cg	ctt	g	ca	g	ac	aa	cc	gg	gc	act	g	cg	cc	ctc	g	at	ac	tt	atg	434
Arg	Ala	Leu	Ala	Asp	Asn	Pro	Gly	Thr	Ala	Pro	Leu	Asp	Thr	Phe	Met							
45								50					55									
acg	ctt	tcc	gaa	tcg	ctg	acc	ggc	aag	aaa	ggg	ctc	agc	cg	gt	atc						482	
Thr	Leu	Ser	Glu	Ser	Leu	Thr	Gly	Lys	Lys	Gly	Leu	Ser	Arg	Val	Ile							
60								65					70							75		
ggc	g	ag	cg	ctg	ctg	cag	ggc	ctg	cag	aag	ggc	tcg	tt	ac	ag	gg					530	
Gly	Glu	Arg	Leu	Leu	Gln	Ala	Leu	Gln	Ala	Leu	Gln	Lys	Gly	Ser	Phe	Lys	Thr	Ala				
80								85					90									
gac	agc	ctg	ccg	cag	ctc	gcc	ggc	g	cg	ctc	g	cg	tcc	g	gt	tcg	ctg	ac			578	
Asp	Ser	Leu	Pro	Gln	Leu	Ala	Gly	Ala	Leu	Ala	Ser	Gly	Ser	Leu	Thr							
95								100					105									
cct	gaa	cag	gaa	tcg	ctc	gca	ctg	ac	atc	ctc	gag	ggc	tgg	tat	ctc						626	
Pro	Glu	Gln	Glu	Ser	Leu	Ala	Leu	Thr	Ile	Leu	Glu	Ala	Trp	Tyr	Leu							
110								115					120									
ggc	atc	gtc	gac	aa	gtc	gt	att	ac	ta	g	g	aa	g	ca	tta	at	tt				674	
Gly	Ile	Val	Asp	Asn	Val	Val	Ile	Thr	Tyr	Glu	Glu	Ala	Leu	Met	Phe							
125								130					135									
ggc	gtc	gt	tcc	gat	ac	ctc	gt	atc	cgt	tcg	tat	tgc	ccc	aa	aa						722	
Gly	Val	Val	Ser	Asp	Thr	Leu	Val	Ile	Arg	Ser	Tyr	Cys	Pro	Asn	Lys							
140								145					150							155		
ccc	ggc	t	tc	tgg	ggc	gac	aa	ccg	atc	gag	agg	caa	ggc	tg	at	ggc					769	
Pro	Gly	Phe	Trp	Ala	Asp	Lys	Pro	Ile	Glu	Arg	Gln	Ala		Met	Ala							
160								165					170									
gat	acc	gat	ac	caa	aag	ggc	gac	gtc	gtc	gt	tt	gga	tcg	gg	gtc						817	
Asp	Thr	Asp	Thr	Gln	Lys	Ala	Asp	Val	Val	Val	Val	Gly	Ser	Gly	Val							
175								180					185									
g	cg	g	tc	g	cg	cat	cag	ctc	g	cg	at	g	gg	a	g	cg	gt				865	
Ala	Gly	Ala	Ile	Val	Ala	His	Gln	Leu	Ala	Met	Ala	Gly	Lys	Ala	Val							
190								195					200									
atc	ct	ct	gaa	ggc	ccg	cg	at	ccg	cg	tgg	gaa	atc	gtc	g							913	
Ile	Leu	Leu	Glu	Ala	Gly	Pro	Arg	Met	Pro	Arg	Trp	Glu	Ile	Val	Glu							
205								210					215									
cgc	tt	cg	cg	aa	cag	cc	gac	aag	at	g	tc	at	g	cg	cc	tac	cc				961	
Arg	Phe	Arg	Asn	Gln	Pro	Asp	Lys	Met	Asp	Phe	Met	Ala	Pro	Tyr	Pro							
220								225					230									
tcg	agc	cc	ttg	ggc	ccg	cat	ccc	gag	ta	g	gc	cc	cc	a	ac	g	ac	ta		1009		

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Ser	Ser	Pro	Trp	Ala	Pro	His	Pro	Glu	Tyr	Gly	Pro	Pro	Asn	Asp	Tyr	
235																250
ctg	atc	ctg	aag	ggc	gag	cac	aag	ttc	aac	tcg	cag	tac	atc	cgc	gcg	1057
Leu	Ile	Leu	Lys	Gly	Glu	His	Lys	Phe	Asn	Ser	Gln	Tyr	Ile	Arg	Ala	
																255
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																265
gtg	ggc	ggc	acg	acg	tgg	cac	tgg	gcc	gcf	tcg	gcf	tgg	cgc	ttc	att	1105
Val	Gly	Gly	Thr	Thr	Trp	His	Trp	Ala	Ala	Ser	Ala	Trp	Arg	Phe	Ile	
																270
																275
																280
ccg	aac	gac	ttc	aag	atg	aag	agc	gtg	tac	ggc	gtc	ggc	cgc	gac	tgg	1153
Pro	Asn	Asp	Phe	Lys	Met	Lys	Ser	Val	Tyr	Gly	Val	Gly	Arg	Asp	Trp	
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																290
																295
ccg	atc	cag	tac	gac	gat	ctc	gag	ccg	tac	tat	cag	cgc	gag	gaa		1201
Pro	Ile	Gln	Tyr	Asp	Asp	Leu	Glu	Pro	Tyr	Tyr	Gln	Arg	Ala	Glu	Glu	
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																305
																310
gag	ctc	ggc	gtg	tgg	ggc	ccg	ggc	ccc	gag	gaa	gat	ctg	tac	tcg	ccg	1249
Glu	Leu	Gly	Val	Trp	Gly	Pro	Gly	Pro	Glu	Glu	Asp	Leu	Tyr	Ser	Pro	
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ccg	aag	cag	ccg	tat	ccg	atg	ccg	ccg	ctg	ccg	tgg	tcg	ttc	aac	gag	1297
Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe	Asn	Glu	
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																340
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cag	acc	atc	aag	acg	ggc	ctg	aac	aac	tac	gat	ccg	aag	ttc	cat	gtc	1345
Gln	Thr	Ile	Lys	Thr	Ala	Leu	Asn	Asn	Tyr	Asp	Pro	Lys	Phe	His	Val	
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gtg	acc	gag	ccg	gtc	ggc	ccg	aac	agc	ccg	ccg	tac	gac	ggc	cgc	ccg	1393
Val	Thr	Glu	Pro	Val	Ala	Arg	Asn	Ser	Arg	Pro	Tyr	Asp	Gly	Arg	Pro	
																365
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act	tgt	tgc	ggc	aac	aac	tgc	atg	ccg	atc	tgc	ccg	atc	ggc	gag		1441
Thr	Cys	Cys	Gly	Asn	Asn	Asn	Cys	Met	Pro	Ile	Cys	Pro	Ile	Gly	Ala	
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																385
																390
atg	tac	aac	ggc	atc	gtg	cac	gtc	gag	aag	gcc	gaa	cgc	gcc	ggc	gcg	1489
Met	Tyr	Asn	Gly	Ile	Val	His	Val	Glu	Lys	Ala	Glu	Arg	Ala	Gly	Ala	
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																400
																405
																410
aag	ctg	atc	gag	aac	gcf	gtc	gtc	tac	aag	ctc	gag	acg	ggc	ccg	gac	1537
Lys	Leu	Ile	Glu	Asn	Ala	Val	Val	Tyr	Lys	Leu	Glu	Thr	Gly	Pro	Asp	
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aag	cgc	atc	gtc	gcf	gcf	ctc	tac	aag	gac	aag	acg	ggc	gcc	gag	cat	1585
Lys	Arg	Ile	Val	Ala	Ala	Leu	Tyr	Lys	Asp	Lys	Thr	Gly	Ala	Glu	His	
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																435
																440
cgc	gtc	gaa	ggc	aag	tat	ttc	gtg	ctc	gcc	gcf	aac	ggc	atc	gag	acg	1633
Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile	Glu	Thr	
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																450
																455
ccg	aag	atc	ctg	ctg	atg	tcc	gcf	aac	cgf	gat	ttc	ccg	aac	ggt	gtc	1681
Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn	Gly	Val	

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460	465	470	
gcg aac agc tcg gac atg gtc ggc cgc aac ctg atg gac cat ccg ggc			1729
Ala Asn Ser Ser Asp Met Val Gly Arg Asn Leu Met Asp His Pro Gly			
475	480	485	490
acc ggc gtg tcg ttc tat gcg agc gag aag ctg tgg ccg ggc cgc ggc			1777
Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly			
495	500	505	
ccg cag gag atg acg tcg ctg atc ggt ttc cgc gac ggt ccg ttc cgc			1825
Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro Phe Arg			
510	515	520	
gcg acc gaa gcg gcg aag aag atc cac ctg tcg aac ctg tcg cgc atc			1873
Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser Arg Ile			
525	530	535	
gac cag gag acg cag aag atc ttc aag gcc ggc aag ctg atg aag ccc			1921
Asp Gln Glu Thr Gln Lys Ile Phe Lys Ala Gly Lys Leu Met Lys Pro			
540	545	550	
gac gag ctc gac gcg cag atc cgc gac cgt tcc gca cgc tac gtg cag			1969
Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr Val Gln			
555	560	565	570
ttc gac tgc ttc cac gaa atc ctg ccg caa ccc gag aac cgc atc gtg			2017
Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg Ile Val			
575	580	585	
ccg agc aag acg gcg acc gat gcg atc ggc att ccg cgc ccc gag atc			2065
Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro Glu Ile			
590	595	600	
acg tat gcg atc gac gac tac gtg aag cgc ggc gcc gcg cat acg cgc			2113
Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His Thr Arg			
605	610	615	
gag gtc tac gcg acc gcc gcg aag gtg ctc ggc ggc acg gac gtc gtg			2161
Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp Val Val			
620	625	630	
ttc aac gac gaa ttc gcg ccg aac aat cac atc acg ggc tcg acg atc			2209
Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser Thr Ile			
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atg ggc gcc gat gcg cgc gac tcc gtc gtc gac aag gac tgc cgc acg			2257
Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys Arg Thr			
655	660	665	
ttc gac cat ccg aac ctg ttc att tcg acg acg gcg acg atg ccg acc			2305
Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ala Thr Met Pro Thr			
670	675	680	
gtc ggt acc gta aac gtg acg ctg acg atc gcc gcg ctc gcg ctg cgg			2353
Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala Leu Arg			
685	690	695	

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atg tcg gac acg ctg aag aag gaa gtc tgacc gtg cgaa aaa tct act ctc 2403
 Met Ser Asp Thr Leu Lys Lys Glu Val Val Arg Lys Ser Thr Leu
 700 705 710
 act ttc ctc atc gcc ggc tgc ctc gcg ttg ccg ggc ttc gcg cgc gcg 2451
 Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu Pro Gly Phe Ala Arg Ala
 715 720 725
 gcc gat gcg gcc gat c 2467
 Ala Asp Ala Ala Asp
 730

<210> 2
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 <212> PRT
 <213> Burkholderia cepacia

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 35 40 45
 Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met Thr Leu Ser Glu Ser
 50 55 60
 Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile Gly Glu Arg Leu Leu
 65 70 75 80
 Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala Asp Ser Leu Pro Gln
 85 90 95
 Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser
 100 105 110
 Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu Gly Ile Val Asp Asn
 115 120 125
 Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe Gly Val Val Ser Asp
 130 135 140
 Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys Pro Gly Phe Trp Ala
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 Asp Lys Pro Ile Glu Arg Gln Ala
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 <212> PRT
 <213> Burkholderia cepacia

<400> 3

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Ala	Val	Ile	Leu	Leu	Glu	Ala	Gly	Pro	Arg	Met	Pro	Arg	Trp	Glu	Ile
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Val	Glu	Arg	Phe	Arg	Asn	Gln	Pro	Asp	Lys	Met	Asp	Phe	Met	Ala	Pro
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Tyr	Pro	Ser	Ser	Pro	Trp	Ala	Pro	His	Pro	Glu	Tyr	Gly	Pro	Pro	Asn
	65					70				75				80	
Asp	Tyr	Leu	Ile	Leu	Lys	Gly	Glu	His	Lys	Phe	Asn	Ser	Gln	Tyr	Ile
					85				90				95		
Arg	Ala	Val	Gly	Gly	Thr	Thr	Trp	His	Trp	Ala	Ala	Ser	Ala	Trp	Arg
					100			105				110			
Phe	Ile	Pro	Asn	Asp	Phe	Lys	Met	Lys	Ser	Val	Tyr	Gly	Val	Gly	Arg
	115					120					125				
Asp	Trp	Pro	Ile	Gln	Tyr	Asp	Asp	Leu	Glu	Pro	Tyr	Tyr	Gln	Arg	Ala
	130					135				140					
Glu	Glu	Glu	Leu	Gly	Val	Trp	Gly	Pro	Gly	Pro	Glu	Glu	Asp	Leu	Tyr
	145				150				155				160		
Ser	Pro	Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe
					165				170				175		
Asn	Glu	Gln	Thr	Ile	Lys	Thr	Ala	Leu	Asn	Asn	Tyr	Asp	Pro	Lys	Phe
					180			185				190			
His	Val	Val	Thr	Glu	Pro	Val	Ala	Arg	Asn	Ser	Arg	Pro	Tyr	Asp	Gly
					195			200			205				
Arg	Pro	Thr	Cys	Cys	Gly	Asn	Asn	Asn	Cys	Met	Pro	Ile	Cys	Pro	Ile
						210		215			220				
Gly	Ala	Met	Tyr	Asn	Gly	Ile	Val	His	Val	Glu	Lys	Ala	Glu	Arg	Ala
	225					230				235			240		
Gly	Ala	Lys	Leu	Ile	Glu	Asn	Ala	Val	Val	Tyr	Lys	Leu	Glu	Thr	Gly
					245			250			255				
Pro	Asp	Lys	Arg	Ile	Val	Ala	Ala	Leu	Tyr	Lys	Asp	Lys	Thr	Gly	Ala
					260			265			270				
Glu	His	Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile
					275			280			285				
Glu	Thr	Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn
					290			295			300				
Gly	Val	Ala	Asn	Ser	Ser	Asp	Met	Val	Gly	Arg	Asn	Leu	Met	Asp	His
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Pro	Gly	Thr	Gly	Val	Ser	Phe	Tyr	Ala	Ser	Glu	Lys	Leu	Trp	Pro	Gly

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325	330	335
Arg Gly Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro		
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Phe Arg Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser		
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Arg Ile Asp Gln Glu Thr Gln Lys Ile Phe Lys Ala Gly Lys Leu Met		
370	375	380
Lys Pro Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr		
385	390	395
395	400	
Val Gln Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg		
405	410	415
Ile Val Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro		
420	425	430
Glu Ile Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His		
435	440	445
Thr Arg Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp		
450	455	460
Val Val Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser		
465	470	475
475	480	
Thr Ile Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys		
485	490	495
Arg Thr Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ser Ala Thr Met		
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Pro Thr Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala		
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Leu Arg Met Ser Asp Thr Leu Lys Lys Glu Val		
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<210> 4

<211> 27

<212> PRT

<213> Burkholderia cepacia

<400> 4

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<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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28

<210> 6

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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29

<210> 7

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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catgccatgg cacacaacga caacact

27

<210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 8

cccaagcttg ggtcagactt ccttcttcag c

31

<210> 9

<211> 16

<212> PRT

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<213> Burkholderia cepacia

<400> 9

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<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus

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<221> UNSURE

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<223> Xaa=unknown

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Xaa	Xaa	Xaa	Asp	Cys	Xaa	Ala	Cys	His							
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<210> 11

<211> 2410

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (673)..(1950)

<400> 11

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 agccgcgaag aagatccatc tgcgaaacat gtccccgcata accaggaga cgcagaagat 180
 cttaaggccc ggcaaactga tgaagcacga ggagctcgac ggcgcagatcc ggcgaccgttc 240
 cgcgcgtac gtgcagttcg actgtttcca cggatcccgat cgcgcgaccgat 300
 cgtgccgagc aagacggcca cggacgcgtatcccgat cgcgcgaccgat 360
 gatgcacgtatccatc tacgtgaagc gggcgccgtt gcacacgcgc gagggttacgtatccatc cgcgcgaccgat 420
 gaagggtgcgtt ggcggcaccg acgtcgatccatc caacgcacgat ttcgcgcgtatccatc acaaccacat 480

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cacgggcgaggatcatgg ggcggatgc acgcgactcg gtcgtcgaca aggactgccg 540
 cacgttcgac catccgaacc tggcccttc gaggcagctcg acgatgccga ccgtcggtac 600
 ggtgaacgtg acgctgacga tcgcggcgct cgcgctgccc atgtcgacaa cgctgaagaa 660
 ggaagtctga cc gtg cgg aaa tct act ctc acc ttc ctc ctc gcc ggc tgc 711
 Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys
 1 5 10
 ctc gcg ctg ccc ggc ctc gca cgc gcg gcc gat tcg gcc gat ccg gcg 759
 Leu Ala Leu Pro Gly Leu Ala Arg Ala Ala Asp Ser Ala Asp Pro Ala
 15 20 25
 cat gtc aag cgc ggc gaa tac ctc gcc gtc gcg ggc gac tgc atg gca 807
 His Val Lys Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala
 30 35 40 45
 tgc cac acc gcg aag ggc ggc aag ccg ttc gcg ggc ggc ctc ggc atg 855
 Cys His Thr Ala Lys Gly Gly Lys Pro Phe Ala Gly Gly Leu Gly Met
 50 55 60
 ccg gtg ccg atg ctc ggc aag atc tat acg agc aac atc aca ccg gat 903
 Pro Val Pro Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp
 65 70 75
 ccc gat acc ggc atc ggc aac tgg acg ttc gag gac ttc gag ccg gcg 951
 Pro Asp Thr Gly Ile Gly Asn Trp Thr Phe Glu Asp Phe Glu Arg Ala
 80 85 90
 gtg cgg cac ggc gta tcg aag aac ggc gac aac ctg tac ccg gcg atg 999
 Val Arg His Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met
 95 100 105
 ccg tac gtg tcg tac gcg aag atc aac gac gac gac gtg caa gcg ctg 1047
 Pro Tyr Val Ser Tyr Ala Lys Ile Asn Asp Asp Asp Val Gln Ala Leu
 110 115 120 125
 tac gcg tac ttc atg cac ggc gtc gaa ccg gtc aag cag gcg ccg ccg 1095
 Tyr Ala Tyr Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro
 130 135 140
 aag aac gag atc ccc gcg ctg ctg agc atg cgc tgg ccg ctg aag atc 1143
 Lys Asn Glu Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile
 145 150 155
 tgg aac tgg ctg ttc ctg aag gac ggc gtc tac cag ccg aag ccc gag 1191
 Trp Asn Trp Leu Phe Leu Lys Asp Gly Val Tyr Gln Pro Lys Pro Glu
 160 165 170
 cag agc gcc gag tgg aac cgc ggc gcc tat ctc gtg cag ggc ctc gcg 1239
 Gln Ser Ala Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala
 175 180 185
 cac tgc agc acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag 1287
 His Cys Ser Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys
 190 195 200 205
 tcg ctc gac gaa acg ggc ggc agc ttc ctg tcg ggc tcg gtg ctc gcg 1335

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aatccggtgtc gcgcacgccc cgcatcgtt tcgttgatcg agaccatgac accgaaccaa 2140
ccgtttctcg cgtcccagcg cgatgtgctg ctgcgtctgt cccgaatctt gctcgtgatc 2200
ctgttcgtga tggtcggctg gaagaagatt atcgacttct ccggtaacgat cgcgttcatg 2260
ggcagcggagg gcgcgcggc gccgatcatc tcggcggcga tctccgtctgt gatggagctc 2320
atcggtcgaa ttgcgatctt cgtcggtttc cagacgcggc cgctcgcgct gtgtcgtcg 2380
ctgticacacga tcggiaccgg catcatcgcc 2410

〈210〉 12

211 <211> 425

<212> PRT

<213> *Burkholderia cepacia*

<400> 12

Val	Arg	Lys	Ser	Thr	Leu	Thr	Phe	Leu	Leu	Ala	Gly	Cys	Leu	Ala	Leu
1				5					10					15	
Pro	Gly	Leu	Ala	Arg	Ala	Ala	Asp	Ser	Ala	Asp	Pro	Ala	His	Val	Lys
				20				25					30		
Arg	Gly	Glu	Tyr	Leu	Ala	Val	Ala	Gly	Asp	Cys	Met	Ala	Cys	His	Thr
					35			40			45				
Ala	Lys	Gly	Gly	Lys	Pro	Phe	Ala	Gly	Gly	Leu	Gly	Met	Pro	Val	Pro
					50			55			60				
Met	Leu	Gly	Lys	Ile	Tyr	Thr	Ser	Asn	Ile	Thr	Pro	Asp	Pro	Asp	Thr
65				70					75					80	
Gly	Ile	Gly	Asn	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala	Val	Arg	His
					85				90					95	
Gly	Val	Ser	Lys	Asn	Gly	Asp	Asn	Leu	Tyr	Pro	Ala	Met	Pro	Tyr	Val
			100					105					110		
Ser	Tyr	Ala	Lys	Ile	Asn	Asp	Asp	Asp	Val	Gln	Ala	Leu	Tyr	Ala	Tyr
				115				120					125		
Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro	Lys	Asn	Glu
				130			135					140			
Ile	Pro	Ala	Leu	Leu	Ser	Met	Arg	Trp	Pro	Leu	Lys	Ile	Trp	Asn	Trp
145					150				155					160	
Leu	Phe	Leu	Lys	Asp	Gly	Val	Tyr	Gln	Pro	Lys	Pro	Glu	Gln	Ser	Ala
					165				170					175	
Glu	Trp	Asn	Arg	Gly	Ala	Tyr	Leu	Val	Gln	Gly	Leu	Ala	His	Cys	Ser
					180			185					190		
Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys	Ser	Leu	Asp
					195			200					205		
Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ser	Gly	Ser	Val	Leu	Ala	Gly	Trp	Asp
					210			215			220				
Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	Gly	Trp	Thr
					225			230			235				240

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Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Leu
 245 250 255
 Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Ile Glu His Ser Phe Ser
 260 265 270
 Lys Met Thr Glu Ala Asp Ile Gly Gly Pro Met Ala Glu Ala Ile Glu
 275 280 285
 His Ser Phe Ser Lys Met Thr Glu Ala Asp Ile Gly Arg Ser Ser Trp
 290 295 300
 Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala
 305 310 315 320
 Ser Ser Gly Ile Asp Pro Ala Pro Leu Tyr Leu Gly Asn Cys Ala Thr
 325 330 335
 Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Pro
 340 345 350
 Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Thr Asn Leu Val
 355 360 365
 Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ala Gly Ser Glu Asp Val
 370 375 380
 Gly Met Pro Ala Phe Arg His Glu Leu Ser Asp Ala Gln Ile Ala Ala
 385 390 395 400
 Leu Thr Asn Tyr Leu Thr Gly Gln Phe Gly Asn Pro Ala Ala Lys Val
 405 410 415
 Thr Glu Gln Asp Val Ala Lys Leu Arg
 420 425

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

tgcaccgtgc ggaaatctac tcctcact

27

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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<400> 14

actttccttct tcagcgtgtc cgacatc

27

<210> 15

<211> 1441

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (121)..(1398)

<400> 15

tccgaacctg	ttcatttcga	gcagcgcgac	gatgccgacc	gtcggtaccc	taaacgtgac	60											
gctgacgatc	gccgcgcctcg	cgctgcggat	gtcggacacg	ctgaagaagg	aagtctgacc	120											
gtg	cgg	aaa	tct	act	ctc	act	ttc	ctc	atc	gcc	ggc	tgc	ctc	gct	ttg	168	
Val	Arg	Lys	Ser	Thr	Leu	Thr	Phe	Leu	Ile	Ala	Gly	Cys	Leu	Ala	Leu		
1	5			10					15								
ccg	ggc	ttc	gct	cg	cg	gct	gat	gct	gct	gat	ccg	gct	ctg	gtc	aag	216	
Pro	Gly	Phe	Ala	Arg	Ala	Ala	Asp	Ala	Ala	Asp	Pro	Ala	Leu	Val	Lys		
20		25								30							
cgc	ggc	gaa	tac	ctc	gct	acc	gcc	atg	ccg	gta	ccg	atg	ctc	ggc	aag	264	
Arg	Gly	Glu	Tyr	Leu	Ala	Thr	Ala	Met	Pro	Val	Pro	Met	Leu	Gly	Lys		
35		40								45							
atc	tac	acg	agc	aac	atc	acg	ccc	gat	ccc	gat	acg	ggc	gac	tgc	atg	312	
Ile	Tyr	Thr	Ser	Asn	Ile	Thr	Pro	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Met		
50		55								60							
gcc	tgc	cac	acc	gtg	aag	ggc	ggc	aag	ccg	tac	gct	ggc	ggc	ctt	ggc	360	
Ala	Cys	His	Thr	Val	Lys	Gly	Gly	Lys	Pro	Tyr	Ala	Gly	Gly	Leu	Gly		
65		70								75				80			
ggc	atc	ggc	aaa	tgg	acg	ttc	gag	gac	ttc	gag	ccg	gct	gtg	cg	cac	408	
Gly	Ile	Gly	Lys	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala	Val	Arg	His		
85		90								95							
ggc	gtg	tcg	aag	aac	ggc	gac	aac	ctg	tat	ccg	gct	atg	ccg	tac	gtg	456	
Gly	Val	Ser	Lys	Asn	Gly	Asp	Asn	Leu	Tyr	Pro	Ala	Met	Pro	Tyr	Val		
100		105								110							
tcg	tac	gct	aag	atc	aag	gac	gac	gac	gta	ccg	gct	ctg	tac	gcc	tac	504	
Ser	Tyr	Ala	Lys	Ile	Lys	Asp	Asp	Asp	Asp	Val	Arg	Ala	Leu	Tyr	Ala	Tyr	
115		120								125							
ttc	atg	cac	ggc	gtc	gag	ccg	gtc	aag	cag	gct	ccg	ccg	aag	aac	gag	552	
Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro	Lys	Asn	Glu		
130		135								140							

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atc cca gcg ctg cta agc atg cgc tgg ccg ctg aag atc tgg aac tgg	600
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp	
145 150 155 160	
ctg ttc ctg aag gac ggc ccg tac cag ccg aag ccg tcg cag agc gcc	648
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala	
165 170 175	
gaa tgg aat cgc ggc gcg tat ctg gtg cag ggt ctc gcg cac tgc agc	696
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser	
180 185 190	
acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag tcg ctc gac	744
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp	
195 200 205	
gaa acc ggc ggc agc ttc ctc gcg ggg tcg ggt ctc gcc ggc tgg gac	792
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp	
210 215 220	
ggc tac aac atc acg tcg gac ccg aat gcg ggg atc ggc agc tgg acg	840
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr	
225 230 235 240	
cag cag cag ctc gtg cag tat ttg cgc acc ggc agc gtg ccg ggc gtc	888
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val	
245 250 255	
gcg cag gcg gcc ggg ccg atg gcc gag gcg gtc gag cac agc ttc tcg	936
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser	
260 265 270	
aag atg acc gaa gcg gac atc ggt gcg atc gcc acg tac gtc cgc acg	984
Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr	
275 280 285	
gtg ccg gcc gtt gcc gac agc aac gcg aag cag ccg cgg tcg tcg tgg	1032
Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp	
290 295 300	
ggc aag ccg gcc gag gac ggg ctg aag ctg cgc ggt gtc gcg ctc gcg	1080
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala	
305 310 315 320	
tcg tcg ggc atc gat ccg gcg cgg ctg tat ctc ggc aac tgc gcg acg	1128
Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr	
325 330 335	
tgc cac cag atg cag ggc aag ggc acg ccg gac ggc tat tac ccg tcg	1176
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser	
340 345 350	
ctg ttc cac aac tcc acc gtc ggc gcg tcg aat ccg tcg aac ctc gtg	1224
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val	
355 360 365	
cag gtg atc ctg aac ggc gtg cag cgc aag atc ggc agc gag gat atc	1272

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Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ile	Gly	Ser	Glu	Asp	Ile	
370						375					380					
ggg	atg	ccc	gct	ttc	cgc	tac	gat	ctg	aac	gac	gcg	cag	atc	gcc	gcg	1320
Gly	Met	Pro	Ala	Phe	Arg	Tyr	Asp	Leu	Asn	Asp	Ala	Gln	Ile	Ala	Ala	
385								390			395			400		
ctg	acg	aac	tac	gtg	acc	gcg	cag	ttc	ggc	aat	ccg	gcg	gcg	aag	gtg	1368
Leu	Thr	Asn	Tyr	Val	Thr	Ala	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val	
								405		410			415			
acg	gag	cag	gac	gtc	gcg	aag	ctg	cgc	tga	catagtcggg	cgccgccgaca					1418
Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg								
								420		425						
cggcgcaacc	gataggacag	gag														1441

<210> 16

<211> 425

<212> PRT

<213> Burkholderia cepacia

<400> 16

Val	Arg	Lys	Ser	Thr	Leu	Thr	Phe	Leu	Ile	Ala	Gly	Cys	Leu	Ala	Leu	
1					5				10					15		
Pro	Gly	Phe	Ala	Arg	Ala	Ala	Asp	Ala	Ala	Asp	Pro	Ala	Leu	Val	Lys	
								20		25			30			
Arg	Gly	Glu	Tyr	Leu	Ala	Thr	Ala	Met	Pro	Val	Pro	Met	Leu	Gly	Lys	
								35		40			45			
Ile	Tyr	Thr	Ser	Asn	Ile	Thr	Pro	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Met	
								50		55			60			
Ala	Cys	His	Thr	Val	Lys	Gly	Gly	Lys	Pro	Tyr	Ala	Gly	Gly	Leu	Gly	
								65		70			75		80	
Gly	Ile	Gly	Lys	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala	Val	Arg	His	
								85		90			95			
Gly	Val	Ser	Lys	Asn	Gly	Asp	Asn	Leu	Tyr	Pro	Ala	Met	Pro	Tyr	Val	
								100		105			110			
Ser	Tyr	Ala	Lys	Ile	Lys	Asp	Asp	Asp	Val	Arg	Ala	Leu	Tyr	Ala	Tyr	
								115		120			125			
Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro	Lys	Asn	Glu	
								130		135			140			
Ile	Pro	Ala	Leu	Leu	Ser	Met	Arg	Trp	Pro	Leu	Lys	Ile	Trp	Asn	Trp	
								145		150			155		160	
Leu	Phe	Leu	Lys	Asp	Gly	Pro	Tyr	Gln	Pro	Lys	Pro	Ser	Gln	Ser	Ala	
								165		170			175			
Glu	Trp	Asn	Arg	Gly	Ala	Tyr	Leu	Val	Gln	Gly	Leu	Ala	His	Cys	Ser	
								180		185			190			

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Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp
 195 200 205
 Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp
 210 215 220
 Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr
 225 230 235 240
 Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val
 245 250 255
 Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser
 260 265 270
 Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr
 275 280 285
 Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp
 290 295 300
 Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala
 305 310 315 320
 Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr
 325 330 335
 Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser
 340 345 350
 Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val
 355 360 365
 Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile Gly Ser Glu Asp Ile
 370 375 380
 Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala
 385 390 395 400
 Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val
 405 410 415
 Thr Glu Gln Asp Val Ala Lys Leu Arg
 420 425

<210> 17

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: heme binding motif

<220>

<221> UNSURE

<222> (2, 3)

<223> Xaa=unknown

<400> 17
Cys Xaa Xaa Cys His
1 5

<210> 18
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18 27
catgccatgg cacacaacga caacact

<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19 31
cccaagcttg ggtcagactt ccttcttcag c